Background paper to ASTA Position Statement on the Use of Genetic Data in Testing for Distinctness, Uniformity and Stability (DUS) under UPOV

Introduction

The Convention of the International Union for the Protection of New Varieties of Plants (UPOV) provides a legal framework for granting intellectual property protection on individual, novel plant varieties based on the qualities of Distinctness, Uniformity, and Stability (DUS). This legal framework is implemented as Plant Breeders' Rights/Plant Variety Protection (PBR/PVP) laws in various jurisdictions. While morphological characteristics remain central to establishing DUS, genetic data has become increasingly useful.

Updating ASTA's 2009 Position Statement

This ASTA position statement updates and replaces ASTA's 2009 "Position Statement on the Use of Molecular Markers in Testing for Distinctness, Uniformity, and Stability (DUS)." The updated statement accounts for the continuing technological advances in genetic knowledge and corresponding analytical tools by broadening the scope from molecular markers to "genetic data." The updated statement continues to address the important role of genetic data, including molecular markers, in strengthening DUS determinations and is consistent with international discussions pertaining to genetic data.

The 2021 position statement also presents new research, including the publication of the peerreviewed journal article, "Single nucleotide polymorphisms facilitate distinctness-uniformitystability testing of soybean cultivars for plant variety protection," in *Crop Science*¹. The work described in this paper, conducted by some ASTA member companies, establishes a threshold using genetic data for augmenting DUS in soybeans and is an illustrative example of an approach that can be considered for other crops.

Why and How are Genetic Data useful in examining DUS?

When the UPOV process was first established in 1961, physically observable morphological characteristics such as leaf shape, flower color, or time of flowering were the only means available to establish distinctness in plant varieties. For certain crops, it has become increasingly difficult to evaluate distinctness based upon morphology alone. These difficulties are compounded by genotype by environment (GxE) interactions that affect expression of characteristics in plants. Additionally, burgeoning variety reference collections means that it takes more time and resources to collect and compare morphological information from a new variety relative to varieties of common knowledge.

As an example, soybeans are a crop which benefits from use of genetic data. Breeders of soybeans have sought to maintain similar gross morphology from variety to variety to meet market expectations of crop appearance, which leads to minimal variation in morphological characteristics to use in determination of Distinctness. A breeding target such as yield, which is a primary commercial driver for soybean breeders and is often the primary difference to

¹ Achard, F, Butruille, M, Madjarac, S., et al. Single nucleotide polymorphisms facilitate distinctness-uniformity-stability testing of soybean cultivars for plant variety protection. *Crop Science*. 2020; 60: 2280–2303. https://doi.org/10.1002/csc2.20201

demonstrate varietal improvement, is not an accepted characteristic for UPOV DUS testing. Differences in the environments where soybeans varieties are grown also impact the expression and presentation of morphological characteristics.

The use of genetic data has expanded and become mainstream across the plant breeding industry in recent years and deserves to be effectively incorporated in DUS determination for plant variety rights. The attributes of genetic data which make it particularly valuable in breeding and in plant science in general, include: high discriminatory power, high repeatability, less vulnerable to variability due to GxE interaction, independent of growth stage, low cost, and amenability to searchable databases. In addition, genetic data could facilitate harmonization among PVP authorities around the globe.

The ASTA Position Statement on the Use of Genetic Data in Testing for Distinctness, Uniformity and Stability (DUS) under UPOV provides suggestions for how genetic data should be collected and used effectively.

What are Genetic Data?

For the purposes of this updated Position Statement, ASTA defines "genetic data" as the analysed output from DNA-based genetic characterization of a variety. Examples of genetic data include molecular marker profiles, such as from using single nucleotide polymorphisms (SNPs) or microsatellites (short tandem repeats or STRs). Currently, SNP profiles are the most used type of genetic data due to the abundance of SNPs in the genome and the availability of high-throughput analytical tools such as SNP arrays. While the availability of genetic data is currently not equal across crops, advances in technology with corresponding decline in costs of genetic sequencing and synthesis is leading to more plant genomes being published. As a result, larger volumes of analysed genetic data are available today.

Emerging Issues

Genetic characterization of plant varieties is accepted by UPOV under specific circumstances of the DUS examination process. Several UPOV members already utilize genetic data within the DUS process for certain crops. Presently, some national plant variety protection offices are determining the extent to which genetic data may be used in DUS testing and Plant Variety Protection applications.

In many jurisdictions, the confidentiality status of genetic data submitted to national PVP offices has not yet been fully determined. Certain genetic data may reveal confidential business information or trade secrets, and breeding organizations have expressed desire that such data remain confidential and are not published publicly. In the case of the *Crop Science* paper, SNP data were generated from publicly available sources to establish a threshold. Under this approach, a breeding organization would submit information as to whether or not their plant variety meets that threshold, rather than submitting their genetic data directly to the PVPO for analysis.